

### **INPUT SET: S36943.raw**

**This Raw Listing contains the General Information Section and up to the first 5 pages.**

**SEQUENCE LISTING**

3 (1) General Information:

4  
5 (i) APPLICANT: BAYLOR COLLEGE OF MEDICINE  
6  
7 SMITH, JAMES R.  
8 DRUTZ, DAVID J.  
9 WILSON, DEBORAH R.  
ZUMSTEIN, LOUIS A.

(ii) TITLE OF INVENTION: SENESCENT CELL DERIVED INHIBITORS OF DNA SYNTHESIS

14 (iii) NUMBER OF SEQUENCES: 36

15 (iv) CORRESPONDENCE ADDRESS:

17 (A) ADDRESSEE: ROGERS & WELLS  
18 (B) STREET: 200 PARK AVENUE  
19 (C) CITY: NEW YORK  
20 (D) STATE: NEW YORK  
21 (E) COUNTRY: USA  
22 (F) ZIP: 10166

24 (v) COMPUTER READABLE FORM:

25 (A) MEDIUM TYPE: Floppy disk  
26 (B) COMPUTER: IBM PC compatible  
27 (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
28 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

30 (vi) CURRENT APPLICATION DATA:

31 (A) APPLICATION NUMBER:10/008,960  
32 (B) FILING DATE: 07-DEC-2001  
33 (C) CLASSIFICATION:

10 □ APPLICATION NUMBER:US 08 327,874  
38 □ B, FILING DATE

(VII) PERIODIC AFFILIATION DATA:

(A) APPLICATION NUMBER: US 07/808,523  
(B) FILING DATE: 16-DEC-1991

46 (vii) PRIOR APPLICATION DATA:

**ENTERED**

**RAW SEQUENCE LISTING  
PATENT APPLICATION US/10/008,960**DATE: 12/10/2002  
TIME: 10:27:50**INPUT SET: S36943.raw**

47 (A) APPLICATION NUMBER: US 07/970,462  
48 (B) FILING DATE: 02-NOV-1992  
49  
50 (vii) PRIOR APPLICATION DATA:  
51 (A) APPLICATION NUMBER: US 08/113,372  
52 (B) FILING DATE: 30-AUG-1993  
53  
54 (vii) PRIOR APPLICATION DATA:  
55 (A) APPLICATION NUMBER: US 08/153,564  
56 (B) FILING DATE: 17-NOV-1993  
57  
58 (vii) PRIOR APPLICATION DATA:  
59 (A) APPLICATION NUMBER: US 08/203,535  
60 (B) FILING DATE: 25-FEB-1994  
61  
62 (vii) PRIOR APPLICATION DATA:  
63 (A) APPLICATION NUMBER: US 08/229,420  
64 (B) FILING DATE: 15-APR-1994  
65  
66 (vii) PRIOR APPLICATION DATA:  
67 (A) APPLICATION NUMBER: US 08/274,535  
68 (B) FILING DATE: 13-JUL-1994  
69  
70 (vii) PRIOR APPLICATION DATA:  
71 (A) APPLICATION NUMBER: PCT US94/09700  
72 (B) FILING DATE: 26-AUG-1994  
73  
74 (vii) PRIOR APPLICATION DATA:  
75 (A) APPLICATION NUMBER: 08/327,874  
76 (B) FILING DATE: 24-OCT-1994  
77  
78 (viii) ATTORNEY/AGENT INFORMATION:  
79 (A) NAME: NORTON, GERARD P.  
80 (B) REGISTRATION NUMBER: 36,621  
81 (C) REFERENCE/DOCKET NUMBER: 3634-8-CIP10  
82  
83 (ix) TELECOMMUNICATION INFORMATION:  
84 (A) TELEPHONE: (212) 878-3148  
85 (B) TELEFAX: (212) 878-8375  
86  
87 (2) INFORMATION FOR SEQ ID NO:1:  
88  
89 (i) SEQUENCE CHARACTERISTICS:  
90 (A) LENGTH: 2106 base pairs  
91 (B) TYPE: nucleic acid  
92 (C) STRANDEDNESS: single  
93 (D) TOPOLOGY: linear  
94  
95 (ii) MOLECULE TYPE: cDNA  
96  
97 (iii) HYPOTHETICAL: NO  
98  
99 (iv) ANTI-SENSE: NO

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100  
 101       (vi) ORIGINAL SOURCE:  
 102           (A) ORGANISM: Homo sapiens  
 103           (G) CELL TYPE: SENESCENT HUMAN CELLS  
 104  
 105       (vii) IMMEDIATE SOURCE:  
 106           (A) LIBRARY: SENESCENT CELL DERIVED CDNA LIBRARY  
 107           (B) CLONE: SDI-1  
 108  
 109       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:  
 110  
 111       CCTGCCGAAG TCAGTTCCTT GTGGAGCCGG AGCTGGGCCG GGATTCGCCG AGGCACCGAG      60  
 112       GCACTCAGAG GAGGCGCCAT GTCAGAACCG GCTGGGGATG TCCGTCAGAA CCCATGCCGC      120  
 113       AGCAAGGCCT GCCGCCGCCT CTTCGGCCA GTGGACAGCG AGCAGCTGAG CGCGACTGT      180  
 114       GATGCGCTAA TGGCGGGCTG CATCAGGAG GCCCGTGAGC GATGGAACCT CGACTTTGTC      240  
 115       ACCGAGACAC CACTGGAGGG TGACTTCGCC TGGGAGCGTG TGCGGGGCC TGGCCTGCC      300  
 116       AAGCTCTACC TTCCCCACGGG GCCCCGGCGA GGCGGGGATG AGTGGGAGG AGGCAGGGCG      360  
 117       CCTGGCACCT CACCTGCTT GCTGCAGGGG ACAGCAGGG AAGACCATGT GGACCTGTCA      420  
 118       CTGTCCTGTA CCCTTGTGCC TCGCTCAGGG GAGCAGGCTG AAGGGTCCCC AGGTGGACCT      480  
 119       GGAGACTCTC AGGGTCGAAA ACCGGGGCAG ACCAGCATGA CAGATTCTA CCACCTCCAAA      540  
 120       CGCCGGCTGA TCTTCTCAA GAGGAAGCCC TAATCCGCC ACAGGAAGCC TGCAGTCCTG      600  
 121       GAAGGCGAG GGCCTCAAAG GCCCGCTCTA CATCTTCTGC CTTAGTCTCA GTTGTGTGT      660  
 122       CTTAATTATT ATTTGTGTT TAATTTAAC ACCTCTCAT GTACATACCC TGGCCGCC      720  
 123       CTGCCCCCA GCCTCTGGCA TTAGAAATTAT TTAAACAAAA ACTAGGCGGT TGAATGAGAG      780  
 124       GTTCTAAGA GTGCTGGCA TTTTTATTAT ATGAAATACT ATTAAAGCC TCCTCATCCC      840  
 125       GTGTTCTCCT TTTCCTCTCT CCCGGAGGTT GGTTGGGCCG GCTTCATGCC AGCTACTTCC      900  
 126       TCCTCCCCAC TTGTCGCTG GGTGGTACCC TCTGGAGGG TGTGGCTCT TCCCCTCGCT      960  
 127       GTCACAGGCG GTTATGAAAT TCACCCCCCTT TCCTGGACAC TCAGACCTGA ATTCTTTTC      1020  
 128       ATTGAGAAG TAAACAGATG GCACCTTGAA GGGGCTCAC CGAGTGGGGG CATCATCCAAA      1080  
 129       AACTTGGAG TCCCCTCACC TCCTCTAAGG TTGGGCAGGG TGACCCCTGAA GTGAGCACAG      1140  
 130       CCTAGGGCTG AGCTGGGGAC CTGGTACCC CTCGGCTCTT GATAACCCCCC TCTGTCTGT      1200  
 131       GAAGGCAGGG GGAAGGTGGG GTCTGGAGC AGACCACCCC GCCTGCCCTC ATGGCCCTC      1260  
 132       TGACCTGCAC TGGGGAGCCC GTCTCAGTGT TGAGCCTTTT CCCTCTTGG CTCCCCCTGTA      1320  
 133       CCTTTGAGG AGCCCCAGCT ACCCTCTTC TCCAGCTGGG CTCTGCAATT CCCCTCTGCT      1380  
 134       GCTGTCCTC CCCCTTGTCC TTTCCTTCA GTACCCCTCTC AGCTCCAGGT GGCTCTGAGG      1440  
 135       TGCCTGTCCC ACCCCCCACCC CCAGCTCAAT GGACTGGAAG GGGAGGGAC ACACAAGAAG      1500  
 136       AAGGGCACCC TAGTTCTACC TCAGGCAGCT CAAGCAGCGA CGGCCCCCTC CTCTAGCTGT      1560  
 137       GGGGGTGAGG GTCCCCTGAG GTGGCACAGG CCCCCTTGAG TGGGGTTATC TCTGTGTAG      1620  
 138       GGGTATATGA TGGGGGAGTA GATCTTCTA GGAGGGAGAC ACTGGCCCT CAAATCGTCC      1680  
 139       AGCGACCTTC CTCATCCACC CCATCCCCTC CCAGTTCTCATT GCACCTTGAT TAGCAGCGGA      1740  
 140       ACAAGGAGTC AGACATTTA AGATGGTGGC AGTAGAGGCT ATGGACAGGG CATGCCACGT      1800  
 141       GGGCTCATAT GGGGCTGGGA GTAGTTGTCT TTCTGGCAC TAACGTTGAG CCCCTGGAGG      1860  
 142       CACTGAAGTG CTTAGTGTAC TTGGAGTATT GGGGTCTGAC CCAAAACACC TTCCAGCTCC      1920  
 143       TGTAAACATAC TGGCCTGGAC TGTTTTCTCT CGGCTCCCCA TGTGTCTGG TTCCCGTTTC      1980  
 144       TCCAGCTAGA TTGTAAATT GTGGAGGCGA TGGAGTAAAGT TGTGTGTGT TGTGTGTCTT      2040  
 145       TCACAGCTCC TCCCACAATG CTGATATACA GCAGGTGCTC AATAAACGAT TCTTGTGAA      2106  
 146       AAAAAAA  
 147  
 148       (2) INFORMATION FOR SEQ ID NO:2:  
 149           (i) SEQUENCE CHARACTERISTICS:  
 150              (A) LENGTH: 164 amino acids  
 151              (B) TYPE: amino acid  
 152              (D) TOPOLOGY: linear

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153  
154       (ii) MOLECULE TYPE: protein  
155  
156       (iii) HYPOTHETICAL: NO  
157  
158       (iv) ANTI-SENSE: NO  
159  
160       (vi) ORIGINAL SOURCE:  
161           (A) ORGANISM: HOMO SAPIENS  
162           (B) STRAIN: SDI-1  
163  
164       (vii) IMMEDIATE SOURCE:  
165           (A) LIBRARY: Senescent cell derived cDNA library  
166  
167       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:  
168  
169       Met Ser Glu Pro Ala Gly Asp Val Arg Gln Asn Pro Cys Gly Ser Lys  
170       1                           5                           10                           15  
171       Ala Cys Arg Arg Leu Phe Gly Pro Val Asp Ser Glu Gln Leu Ser Arg  
172       20                           25                           30  
173       Asp Cys Asp Ala Leu Met Ala Gly Cys Ile Gln Glu Ala Arg Glu Arg  
174       35                           40                           45  
175       Trp Asn Phe Asp Phe Val Thr Glu Thr Pro Leu Glu Gly Asp Phe Ala  
176       50                           55                           60  
177       Trp Glu Arg Val Arg Gly Leu Gly Leu Pro Lys Leu Tyr Leu Pro Thr  
178       65                           70                           75                           80  
179       Gly Pro Arg Arg Gly Arg Asp Glu Leu Gly Gly Arg Arg Pro Gly  
180       85                           90                           95  
181       Thr Ser Pro Ala Leu Leu Gln Gly Thr Ala Glu Glu Asp His Val Asp  
182       100                           105                           110  
183       Leu Ser Leu Ser Cys Thr Leu Val Pro Arg Ser Gly Glu Gln Ala Glu  
184       115                           120                           125  
185       Gly Ser Pro Gly Gly Pro Gly Asp Ser Gln Gly Arg Lys Arg Arg Gln  
186       130                           135                           140  
187       Thr Ser Met Thr Asp Phe Tyr His Ser Lys Arg Arg Leu Ile Phe Ser  
188       145                           150                           155                           160  
189       Lys Arg Lys Pro  
190  
191       (2) INFORMATION FOR SEQ ID NO:3:  
192  
193       (i) SEQUENCE CHARACTERISTICS:  
194           (A) LENGTH: 19 base pairs  
195           (B) TYPE: nucleic acid  
196           (C) STRANDEDNESS: single  
197           (D) TOPOLOGY: linear  
198  
199       (ii) MOLECULE TYPE: cDNA  
200  
201       (iii) HYPOTHETICAL: NO  
202  
203       (iv) ANTI-SENSE: YES  
204  
205       (vi) ORIGINAL SOURCE:

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206             (A) ORGANISM: HOMO SAPIENS
207
208             (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
209
210 AGCCGGTTCT GACATGGCG                               19
211
212             (2) INFORMATION FOR SEQ ID NO:4:
213                 (i) SEQUENCE CHARACTERISTICS:
214                     (A) LENGTH: 12 amino acids
215                     (B) TYPE: amino acid
216                     (D) TOPOLOGY: linear
217
218                 (ii) MOLECULE TYPE: peptide
219
220                 (iii) HYPOTHETICAL: NO
221
222                 (v) FRAGMENT TYPE: N-terminal
223
224                 (vii) IMMEDIATE SOURCE:
225                     (B) CLONE: [His]6 leader peptide
226
227             (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
228
229             Met Arg Gly Ser His His His His His Gly Ala
230                 1           5           10
231
232             (2) INFORMATION FOR SEQ ID NO:5:
233
234                 (i) SEQUENCE CHARACTERISTICS:
235                     (A) LENGTH: 699 base pairs
236                     (B) TYPE: nucleic acid
237                     (C) STRANDEDNESS: single
238                     (D) TOPOLOGY: linear
239
240                 (ii) MOLECULE TYPE: cDNA
241
242                 (iii) HYPOTHETICAL: NO
243
244                 (iv) ANTI-SENSE: NO
245
246                 (vi) ORIGINAL SOURCE:
247                     '(A)' ORGANISM: Schistosoma japonicum
248
249                 (vii) IMMEDIATE SOURCE:
250                     E CLONE GST
251
252             (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5.
253
254 ATGTCGCCATA TACTAGCTTA TTGCAAAATT AACCCCCCTTG TGCAAAACCCAC TCGACTTCTT      60
255 TTGGAATATC TTGAAGAAAA ATATGAAGAG CATTGTATG AGCGCGATGA AGGTGATAAAA      120
256 TGGCGAAACA AAAAGTTCA ATTGGGTTTG GAGTTTCCCA ATCTTCCTTA TTATATTGAT      180
257 GGTGATGTTA AATTAACACA GTCTATGGCC ATCATACGTT ATATAGCTGA CAAGCACAAC      240
258 ATGTTGGGTG GTTGTCCAAA AGAGCGTGCA GAGATTCAA TGCTTGAAGG AGCGGTTTG      300

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**SEQUENCE VERIFICATION REPORT**  
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**SEQUENCE MISSING ITEM REPORT**  
PATENT APPLICATION *US/10/008,960*

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PRIOR APPLICATION DATA More Identifiers Found Than MAX Allowed

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**SEQUENCE CORRECTION REPORT**  
PATENT APPLICATION **US/10/008,960**

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